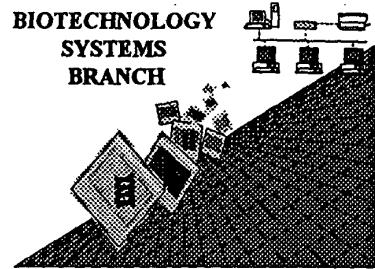# RAW SEQUENCE LISTING
ERROR REPORT

0200

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/507,968

Art Unit / Team No. : 0116

Date Processed by STIC: 3/10/2000

THE ATTACHED PRINTOUT EXPLAINS THE **ERRORS DETECTED.**

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

MARK SPENCER 703-308-4212

Raw Sequence Listing Error Summary

ERROR DETECTED **SUGGESTED   CORRECTION**   SERIAL NUMBER: _09/507,968_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos   The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length   The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid   The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering   between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII   This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES)   **(2) INFORMATION FOR SEQ ID NO:X:**
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES)   **<210> sequence id number**
<400> sequence id number
000

10 _____ Use of n's or **Xaa's**   Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES)   Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or **Xaa**, and which residue n or **Xaa** represents.

11 _____ Use of <213>Organism   Sequence(s) _____ are missing this mandatory field or its response.
(NEW RULES)

12 _____ Use of <220>Feature   Sequence(s) _____ are missing the <220>Feature and associated headings.
(NEW RULES)   Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"   **Please do not us "Copy t Disk" function of PatentIn version 2.0. This causes a corrupted**
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

> **This Raw Listing contains the General
> Information Section and those Sequences
> containing ERRORS.**

1	<110> Yu, Guo-Liang	Does Not Comply
2	Ebner, Reinhard	Corrected Diskette Needed
3	Ni, Jian	
4	Rosen, Craig A.	
5	<120> Neutrokine-alpha and Neutrokine-alpha Splice Variants	
6	<130> PF343P3	
7	<140> US/09/507,968	
8	<141> 2000-02-22	
9	<150> 60/122,388	
10	<151> 1999-03-02	
11	<150> 60/124,097	
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29	<150> 60/142,659	
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35	<150> 60/168,624	
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41	<150> 60/176,015	
42	<151> 2000-01-14	
43	<160> 38	
44	<170> PatentIn Ver. 2.1	

ERRORED SEQUENCES FOLLOW

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        45   <210> 1
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        47   <212> DNA
        48   <213> Homo sapiens      next page
        49   <220>
        50   <221> CDS
        51   <222> (147)..(1001)
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        54        atcaacaaac acagataaca ggaaatgatc cattccctgt ggtcacttat tctaaaggcc 120
        55        ccaaccttca aagttcaagt agtgat atg gat gac tcc aca gaa agg gag cag  173
        56                                Met Asp Asp Ser Thr Glu Arg Glu Gln
        57                                 1               5
        58        tca cgc ctt act tct tgc ctt aag aaa aga gaa gaa atg aaa ctg aag  221
        59        Ser Arg Leu Thr Ser Cys Leu Lys Lys Arg Glu Glu Met Lys Leu Lys
        60         10              15                  20                  25
        61        gag tgt gtt tcc atc ctc cca cgg aag gaa agc ccc tct gtc cga tcc  269
        62        Glu Cys Val Ser Ile Leu Pro Arg Lys Glu Ser Pro Ser Val Arg Ser
        63                         30                  35                  40
        64        tcc aaa gac gga aag ctg ctg gct gca acc ttg ctg ctg gca ctg ctg  317
        65        Ser Lys Asp Gly Lys Leu Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu
        66                     45                  50                  55
        67        tct tgc tgc ctc acg gtg gtg tct ttc tac cag gtg gcc gcc ctg caa  365
        68        Ser Cys Cys Leu Thr Val Val Ser Phe Tyr Gln Val Ala Ala Leu Gln
        69                 60                  65                  70
        70        ggg gac ctg gcc agc ctc cgg gca gag ctg cag ggc cac cac gcg gag  413
        71        Gly Asp Leu Ala Ser Leu Arg Ala Glu Leu Gln Gly His His Ala Glu
        72             75                  80                  85
        73        aag ctg cca gca gga gca gga gcc ccc aag gcc ggc ctg gag gaa gct  461
        74        Lys Leu Pro Ala Gly Ala Gly Ala Pro Lys Ala Gly Leu Glu Glu Ala
        75         90                  95                  100                 105
        76        cca gct gtc acc gcg gga ctg aaa atc ttt gaa cca cca gct cca gga  509
        77        Pro Ala Val Thr Ala Gly Leu Lys Ile Phe Glu Pro Pro Ala Pro Gly
        78                     110                 115                 120
        79        gaa ggc aac tcc agt cag aac agc aga aat aag cgt gcc gtt cag ggt  557
        80        Glu Gly Asn Ser Ser Gln Asn Ser Arg Asn Lys Arg Ala Val Gln Gly
        81                     125                 130                 135
        82        cca gaa gaa aca gtc act caa gac tgc ttg caa ctg att gca gac agt  605
        83        Pro Glu Glu Thr Val Thr Gln Asp Cys Leu Gln Leu Ile Ala Asp Ser
        84                     140                 145                 150
        85        gaa aca cca act ata caa aaa gga tct tac aca ttt gtt cca tgg ctt  653
        86        Glu Thr Pro Thr Ile Gln Lys Gly Ser Tyr Thr Phe Val Pro Trp Leu
        87                     155                 160                 165
        88        ctc agc ttt aaa agg gga agt gcc cta gaa gaa aaa gag aat aaa ata  701
        89        Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu Lys Glu Asn Lys Ile
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90	170			175				180				185		
91	ttg	gtc	aaa	gaa	act	ggt	tac	ttt	ttt	ata	tat	ggt	cag	gtt	tta	tat	749
92	Leu	Val	Lys	Glu	Thr	Gly	Tyr	Phe	Phe	Ile	Tyr	Gly	Gln	Val	Leu	Tyr
93				190				195				200
94	act	gat	aag	acc	tac	gcc	atg	gga	cat	cta	att	cag	agg	aag	aag	gtc	797
95	Thr	Asp	Lys	Thr	Tyr	Ala	Met	Gly	His	Leu	Ile	Gln	Arg	Lys	Lys	Val
96				205				210				215
97	cat	gtc	ttt	ggg	gat	gaa	ttg	agt	ctg	gtg	act	ttg	ttt	cga	tgt	att	845
98	His	Val	Phe	Gly	Asp	Glu	Leu	Ser	Leu	Val	Thr	Leu	Phe	Arg	Cys	Ile
99				220				225				230
100	caa	aat	atg	cct	gaa	aca	cta	ccc	aat	aat	tcc	tgc	tat	tca	gct	ggc	893
101	Gln	Asn	Met	Pro	Glu	Thr	Leu	Pro	Asn	Asn	Ser	Cys	Tyr	Ser	Ala	Gly
102				235				240				245
103	att	gca	aaa	ctg	gaa	gaa	gga	gat	gaa	ctc	caa	ctt	gca	ata	cca	aga	941
104	Ile	Ala	Lys	Leu	Glu	Glu	Gly	Asp	Glu	Leu	Gln	Leu	Ala	Ile	Pro	Arg
105				250				255				260				265
106	gaa	aat	gca	caa	ata	tca	ctg	gat	gga	gat	gtc	aca	ttt	ttt	ggt	gca	989
107	Glu	Asn	Ala	Gln	Ile	Ser	Leu	Asp	Gly	Asp	Val	Thr	Phe	Phe	Gly	Ala
108				270				275				280

E--> 109   ttg aaa ctg ctg tgacctactt acaccatgtc tgtagctatt ttcctccctt   1041
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    111   Leu Lys Leu Leu
    112   285

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W--> 114   1100

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    117   <212> DNA
    118   <213> Homo sapiens
    119   <220>
    120   <221> CDS
    121   <222> (1)..(468)
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124	Arg	Val	Val	Asp	Leu	Ser	Ala	Pro	Pro	Ala	Pro	Cys	Leu	Pro	Gly	Cys
125	1				5					10					15
126	cgc	cat	tct	caa	cat	gat	gat	aat	gga	atg	aac	ctc	aga	aac	aga	act	96
127	Arg	His	Ser	Gln	His	Asp	Asp	Asn	Gly	Met	Asn	Leu	Arg	Asn	Arg	Thr
128				20					25					30
129	tac	aca	ttt	gtt	cca	tgg	ctt	ctc	agc	ttt	aaa	aga	gga	aat	gcc	ttg	144
130	Tyr	Thr	Phe	Val	Pro	Trp	Leu	Leu	Ser	Phe	Lys	Arg	Gly	Asn	Ala	Leu
131				35				40					45
132	gag	gag	aaa	gag	aac	aaa	ata	gtg	gtg	agg	caa	aca	ggc	tat	ttc	ttc	192
133	Glu	Glu	Lys	Glu	Asn	Lys	Ile	Val	Val	Arg	Gln	Thr	Gly	Tyr	Phe	Phe
134		50				55				60
135	atc	tac	agc	cag	gtt	cta	tac	acg	gac	ccc	atc	ttt	gct	atg	ggt	cat	240
136	Ile	Tyr	Ser	Gln	Val	Leu	Tyr	Thr	Asp	Pro	Ile	Phe	Ala	Met	Gly	His
137	65				70				75					80
138	gtc	atc	cag	agg	aag	aaa	gta	cac	gtc	ttt	ggg	gac	gag	ctg	agc	ctg	288

(handwritten annotations in right margin: "format error (see item 1 on Error summary sheet)")

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139        Val Ile Gln Arg Lys Lys Val His Val Phe Gly Asp Glu Leu Ser Leu
140                        85              90              95
141        gtg acc ctg ttc cga tgt att cag aat atg ccc aaa aca ctg ccc aac   336
142        Val Thr Leu Phe Arg Cys Ile Gln Asn Met Pro Lys Thr Leu Pro Asn
143                        100             105             110
144        aat tcc tgc tac tcg gct ggc atc gcg agg ctg gaa gaa gga gat gag   384
145        Asn Ser Cys Tyr Ser Ala Gly Ile Ala Arg Leu Glu Glu Gly Asp Glu
146                        115             120             125
147        att cag ctt gca att cct cgg gag aat gca cag att tca cgc aac gga   432
148        Ile Gln Leu Ala Ile Pro Arg Glu Asn Ala Gln Ile Ser Arg Asn Gly
149                 130             135             140
150        gac gac acc ttc ttt ggt gcc cta aaa ctg ctg taa ctcacttgct         478
151        Asp Asp Thr Phe Phe Gly Ala Leu Lys Leu Leu
152                 145             150             155
153        ggagtgcgtg atccccttcc ctcgtcttct ctgtacctcc gagggagaaa cagacgactg 538
154        gaaaaactaa aagatgggga aagccgtcag cgaaagtttt ctcgtgaccc gttgaatctg 598
155        atccaaacca ggaaatataa cagacagcca caaccgaagt gtgccatgtg agttatgaga 658
156        aacggagccc gcgctcagaa agaccggatg aggaagaccg ttttctccag tcctttgcca 718
157        acacgcaccg caaccttgct ttttgccttg ggtgacacat gttcagaatg cagggagatt 778
158        tccttgtttt gcgatttgcc atgagaagag ggcccacaac tgcaggtcac tgaagcattc 838
159        acgctaagtc tcaggattta ctctcccttc tcatgctaag tacacacacg ctctttca  898
160        ggtaatacta tgggatacta tggaaaggtt gtttgttttt aaatctagaa gtcttgaact 958
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E--> 161   ggcaatagac aaaaatcctt ataaattcaa gtgtaaaata aacttaatta aaaaggttta ~1018
      162   1018 —

E--> 163   agtgtgaaaa aaaaaaaaaa aa   ~1040
      164   1040

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166   <211> 177
167   <212> DNA
168   <213> Mus musculus
169   <400> 38
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W--> 170   mdsaktcccg kgdmkvgydt kgawgcrdgr aatassstam syaaadmrm syrgsataaa 60
W--> 171   gatagvktaa rhssrghrn rragtdvdsa acgcrhshdd ngmkndcad sdtaknkvvr 120
W--> 172   tgyysvytda mghvrkkvhv gdsvtrcmk tnncysaga rgdarnasrn gddtgak   177
E--> 173

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

Line	?	Error/Warning	Original Text
46	E	Input 1100, Calc# Bases 989 differ	<211> 1100
109	E	Wrong Amino Acid Designator	ttg aaa ctg ctg tgacctactt acaccatgtc tgt
109	E	Wrong Amino Acid Designator	ttg aaa ctg ctg tgacctactt acaccatgtc tgt
109	E	Wrong Amino Acid Designator	ttg aaa ctg ctg tgacctactt acaccatgtc tgt
109	E	Wrong Amino Acid Designator	ttg aaa ctg ctg tgacctactt acaccatgtc tgt
109	E	Wrong Amino Acid Designator	ttg aaa ctg ctg tgacctactt acaccatgtc tgt
109	E	Wrong Amino Acid Designator	ttg aaa ctg ctg tgacctactt acaccatgtc tgt
109	E	Wrong Amino Acid Designator	ttg aaa ctg ctg tgacctactt acaccatgtc tgt
109	E	Wrong Amino Acid Designator	ttg aaa ctg ctg tgacctactt acaccatgtc tgt
113	E	Wrong Amino Acid Designator	tctctgtacc tctaagaaga aagaatctaa ctgaaaat
113	E	Wrong Amino Acid Designator	tctctgtacc tctaagaaga aagaatctaa ctgaaaat
113	E	Wrong Amino Acid Designator	tctctgtacc tctaagaaga aagaatctaa ctgaaaat
113	E	Wrong Amino Acid Designator	tctctgtacc tctaagaaga aagaatctaa ctgaaaat
113	E	Wrong Amino Acid Designator	tctctgtacc tctaagaaga aagaatctaa ctgaaaat
113	E	Wrong Amino Acid Designator	tctctgtacc tctaagaaga aagaatctaa ctgaaaat
114	W	Invalid/Missing Amino Acid Numbering	1100
116	E	Input 1040, Calc# Bases 958 differ	<211> 1040
161	E	Wrong Amino Acid Designator	ggcaatagac aaaaatcctt ataaattcaa gtgtaaaa
161	E	Wrong Amino Acid Designator	ggcaatagac aaaaatcctt ataaattcaa gtgtaaaa
161	E	Wrong Amino Acid Designator	ggcaatagac aaaaatcctt ataaattcaa gtgtaaaa
161	E	Wrong Amino Acid Designator	ggcaatagac aaaaatcctt ataaattcaa gtgtaaaa
161	E	Wrong Amino Acid Designator	ggcaatagac aaaaatcctt ataaattcaa gtgtaaaa
161	E	Wrong Amino Acid Designator	ggcaatagac aaaaatcctt ataaattcaa gtgtaaaa
163	E	Wrong Amino Acid Designator	agtgtgaaaa aaaaaaaaaa aa
163	E	Wrong Amino Acid Designator	agtgtgaaaa aaaaaaaaaa aa
163	E	Wrong Amino Acid Designator	agtgtgaaaa aaaaaaaaaa aa
170	W	"N" or "Xaa" used: Feature required	mdsaktcccs kgdmkvgydt kgawgcrdgr aatassst
171	W	"N" or "Xaa" used: Feature required	gatagvktaa rhnssrghrn rragtdvdsa acgcrhsh
172	W	"N" or "Xaa" used: Feature required	tgyysvytda mghvrkkvhv gdsvtrcnmk tnnscysa
173	E	Number of Bases conflict w/ Running Total	25